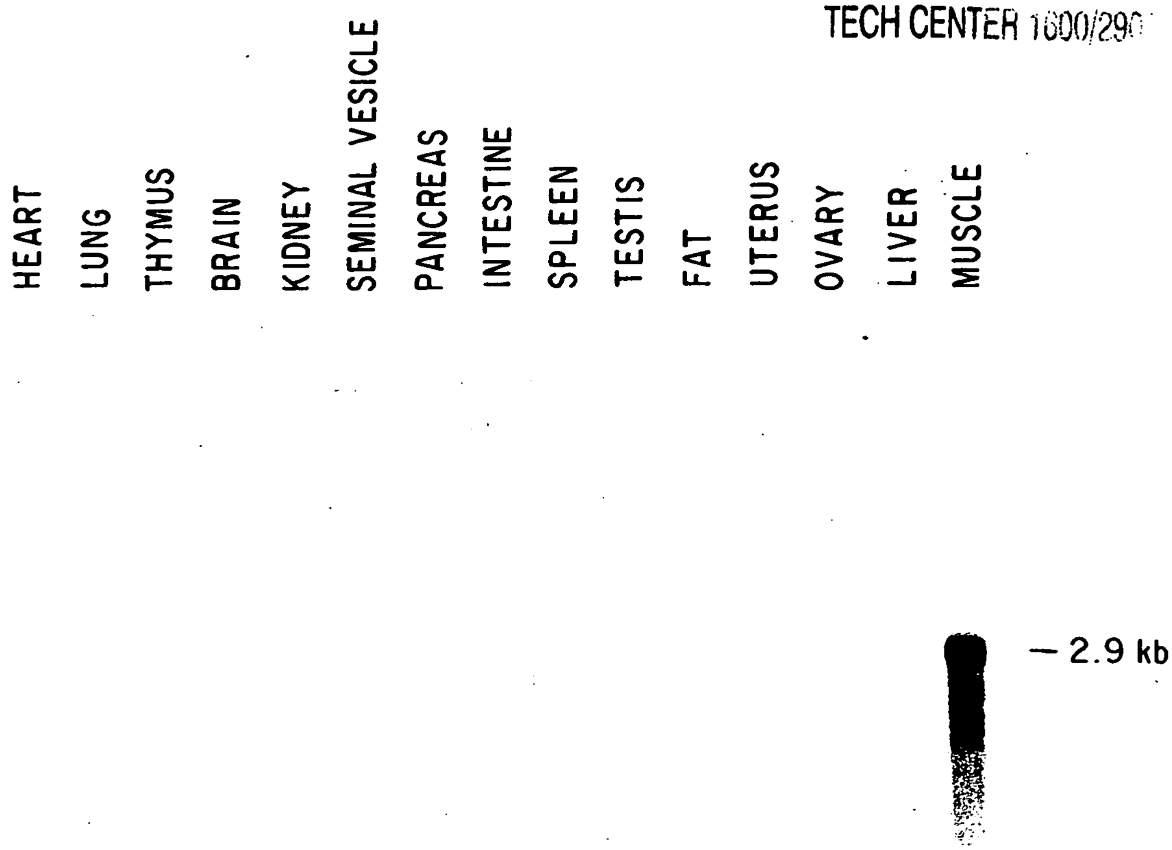

HEART
LUNG
THYMUS
BRAIN
KIDNEY
SEMINAL VESICLE
PANCREAS
INTESTINE
SPLEEN
TESTIS
FAT
UTERUS
OVARY
LIVER
MUSCLE
— 2.9 kb

FIG. 1A

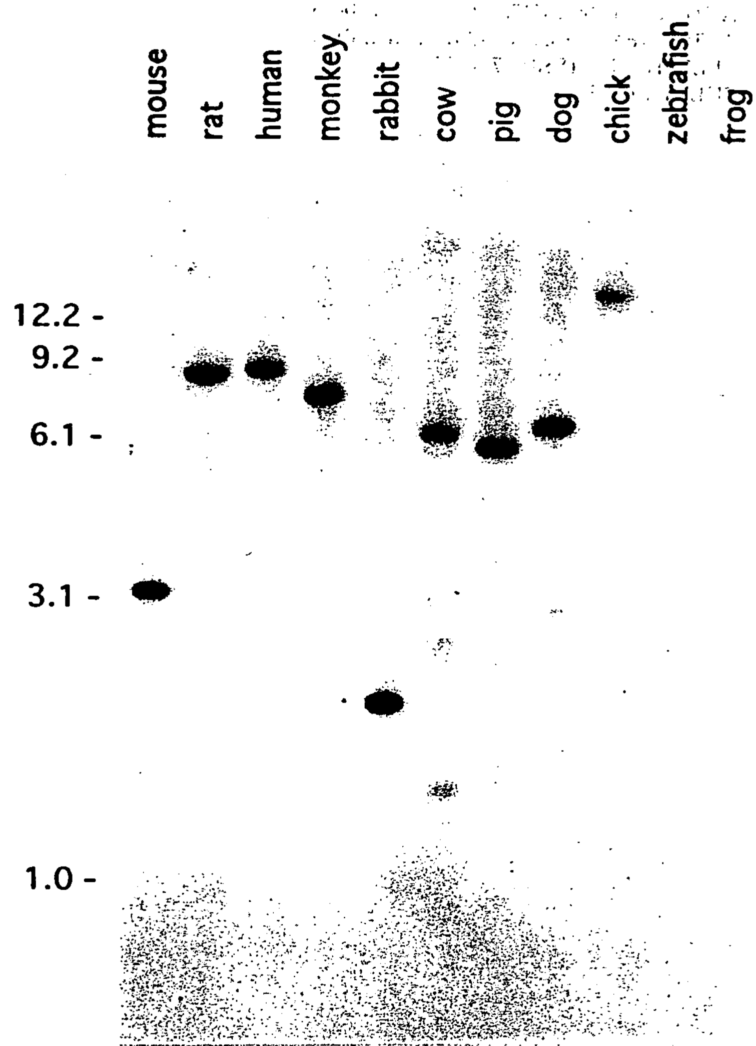

mouse
rat
human
monkey
rabbit
cow
pig
dog
chick
zebrafish
frog
12.2 -
9.2 -
6.1 -
3.1 -
1.0 -

FIG. 1B

```
  1 TTAAGGTAGGAAGGATTTCAGGCTCTATTTACATAATTGTTCTTTCCTTTTCACACAGAA  60
                                                            N
 61 TCCCTTTTTAGAAGTCAAGGTGACAGACACACCCAAGAGGTCCCGGAGAGACTTTGGGCT 120
     P  F  L  E  V  K  V  T  D  T  P [K  R] S [R  R] D  F  G  L
121 TGACTGCGATGAGCACTCCACGGAATCCCGGTGCTGCCGCTACCCCCTCACGGTCGATTT 180
     D  C  D  E  H  S  T  E  S  R  C  C  R  Y  P  L  T  V  D  F
181 TGAAGCCTTTGGATGGGACTGGATTATCGCACCCAAAAGATATAAGGCCAATTACTGCTC 240
     E  A  F  G  W  D  W  I  I  A  P  K  R  Y  K  A  N  Y  C  S
241 AGGAGAGTGTGAATTTGTGTTTTTACAAAAATATCCGCATACTCATCTTGTGCACCAAGC 300
     G  E  C  E  F  V  F  L  Q  K  Y  P  H  T  H  L  V  H  Q  A
301 AAACCCCAGAGGCTCAGCAGGCCCTTGCTGCACTCCGACAAAAATGTCTCCCATTAATAT 360
     N  P  R  G  S  A  G  P  C  C  T  P  T  K  M  S  P  I  N  M
361 GCTATATTTTAATGGCAAAGAACAAATAATATATGGAAAATTCCAGCCATGGTAGTAGA 420
     L  Y  F  N  G  K  E  Q  I  I  Y  G  K  I  P  A  M  V  V  D
421 CCGCTGTGGGTGCTCATGAGCTTTGCATTAGGTTAGAAACTTCCCAAGTCATGGAAGGTC 480
     R  C  G  C  S  *
481 TTCCCCTCAATTTCGAAACTGTGAATTCCTGCAGCCCGGGGGATCCACTAGTTCTAGAGC 540
541 GGCCGCCACC   550
```

FIG. 2A

```
  1 CAAAAAGATCCAGAAGGGATTTTGGTCTTGACTGTGATGAGCACTCAACAGAATCACGAT  60
    [K  R] S [R  R] D  F  G  L  D  C  D  E  H  S  T  E  S  R  C
 61 GCTGTCGTTACCCTCTAACTGTGGATTTTGAAGCTTTTGGATGGGATTGGATTATCGCTC 120
      C  R  Y  P  L  T  V  D  F  E  A  F  G  W  D  W  I  I  A  P
121 CTAAAAGATATAAGGCCAATTACTGCTCTGGAGAGTGTGAATTTGTATTTTTACAAAAAT 180
      K  R  Y  K  A  N  Y  C  S  G  E  C  E  F  V  F  L  Q  K  Y
181 ATCCTCATACTCATCTGGTACACCAAGCAAACCCCAGAGGTTCAGCAGGCCCTTGCTGTA 240
      P  H  T  H  L  V  H  Q  A  N  P  R  G  S  A  G  P  C  C  T
241 CTCCCACAAAGATGTCTCCAATTAATATGCTATATTTTAATGGCAAAGAACAAATAATAT 300
      P  T  K  M  S  P  I  N  M  L  Y  F  N  G  K  E  Q  I  I  Y
301 ATGGGAAAATTCCAGCGATGGTAGTA   326
      G  K  I  P  A  M  V  V
```

FIG. 2B

```
GAA GAT GGG CTG AAT CCC TTT TTA GAA GTC AAA GTA ACA GAC ACA CCC AAG AGG TCC CGG
 E   D   G   L   N   P   F   L   E   V   K   V   T   D   T   P   K   R   S   R

AGA GAC TTT GGG CTT GAC TGT GAT GAA CAC TCC ACG GAA TCG CGG TGC TGT CGC TAC CCC
 R   D   F   G   L   D   C   D   E   H   S   T   E   S   R   C   C   R   Y   P

CTC ACG GTC GAT TTC GAA GCC TTT GGA TGG GAC TGG ATT ATT GCA CCC AAA AGA TAT AAG
 L   T   V   D   F   E   A   F   G   W   D   W   I   I   A   P   K   R   Y   K

GCT AAT TAC TGC TCT GGA GAG TGT GAA TTT GTG TTC TTA CAA AAA TAT CCG CAT ACT CAT
 A   N   Y   C   S   G   E   C   E   F   V   F   L   Q   K   Y   P   H   T   H

CTT GTG CAC CAA GCA AAC CCC AGA GGC TCG GCA GGC CCT TGC TGC ACG CCA ACA AAA ATG
 L   V   H   Q   A   N   P   R   G   S   A   G   P   C   C   T   P   T   K   M

TCT CCC ATT AAT ATG CTA TAT TTT AAT GGC AAA GAA CAA ATA ATA TAT GGG AAA ATT CCA
 S   P   I   N   M   L   Y   F   N   G   K   E   Q   I   I   Y   G   K   I   P

GCC ATG GTA GTA GAC CGG TGT GGG TGC TCG TGA GCT TTG CAT TAG CTT TAA AAT TTC CCA
 A   M   V   V   D   R   C   G   C   S

AAT CGT GGA AGG TCT TCC CCT CGA TTT CGA AAC TGT GAA TTT ATG TAC CAC AGG CTG TAG
```

RAT GDF-8

FIG. 2C

```
TTA GTA GTA AAG GCA CAA TTA TGG ATA TAC TTG AGG CAA GTC CAA AAA CCT ACA ACG GTG
 L   V   V   K   A   Q   L   W   I   Y   L   R   Q   V   Q   K   P   T   T   V

TTT GTG CAG ATC CTG AGA CTC ATT AAG CCC ATG AAA GAC GGT ACA AGA TAT ACT GGA ATT
 F   V   Q   I   L   R   L   I   K   P   M   K   D   G   T   R   Y   T   G   I

GGA TCT TTG AAA CTT GAC ATG AAC CCA GGC ACT GGT ATC TGG CAG AGT ATT GAT GTG AAG
 G   S   L   K   L   D   M   N   P   G   T   G   I   W   Q   S   I   D   V   K

ACA GTG CTG CAA AAT TGG CTC AAA ACG CCT GAA TCC AAT TTA GGC ATC GAA ATA AAA GCT
 T   V   L   Q   N   W   L   K   Q   P   E   S   N   L   G   I   E   I   K   A

TTT GAT GAG ACT GGA CGA GAT CTT GCT GTC ACA TTC CCA GGA CCG GGT GAA GAT GGA TTG
 F   D   E   T   G   R   D   L   A   V   T   F   P   G   P   G   E   D   G   L

AAC CCA TTT TTA GAG GTC AGA GTT ACA GAC ACA CCG AAA CGG TCC CGC AGA GAT TTT GGC
 N   P   F   L   E   V   R   V   T   D   T   P   K   R   S   R   R   D   F   G

CTT GAC TGT GAT GAG CAC TCA ACG GAA TCC CGA TGT TGT CGC TAC CCG CTG ACA GTG GAT
 L   D   C   D   E   H   S   T   E   S   R   C   C   R   Y   P   L   T   V   D

TTC GAA GCT TTT GGA TGG GAC TGG ATT ATA GCA CCT AAA AGA TAC AAA GCC AAT TAC TGC
 F   E   A   F   G   W   D   W   I   I   A   P   K   R   Y   K   A   N   Y   C

TCC GGA GAA TGC GAA TTT GTG TTT CTA CAG AAA TAC CCG CAC ACT CAC CTG GTA CAC CAA
 S   G   E   C   E   F   V   F   L   Q   K   Y   P   H   T   H   L   V   H   Q

GCA AAT CCC AGA GGC TCA GCA GGC CCT TGC TGC ACA CCC ACC AAG ATG TCC CCT ATA AAC
 A   N   P   R   G   S   A   G   P   C   C   T   P   T   K   M   S   P   I   N

ATG CTG TAT TTC AAT GGA AAA GAA CAA ATA ATA TAT GGA AAG ATA CCA GCC ATG GTT GTA
 M   L   Y   F   N   G   K   E   Q   I   I   Y   G   K   I   P   A   M   V   V

GAT CGT TGC GGG TGC TCA TGA GGC TGT CGT GAG ATC CAC CAT TCG ATA AAT TGT GGA AGC
 D   R   C   G   C   S

CAC CAA AAA AAA AAG CTA TAT CCC CTC ATC CAT CTT TGA AAC TGT GAA ATT ACG TAC GCT

AGG CAT TGC C
```

CHICKEN GDF-8

FIG. 2D

zebrafish.nucleotide
[Strand]

```
1    ATGCATTTTA CACAGGTTTT AATTTCTCTA AGTGTATTAA TTGCATGTGG TCCAGTGGGT TATGGAGATA
       M  H  F  T  Q  V  L  I  S  L  S  V  L  I  A  C  G  P  V  G  Y  G  D
71   TAACGGCGCA CCAGCAGCCT TCCACAGCCA CGGAGGAAAG CGAGCTGTGT TCCACATGTG AGTTCAGACA
      I  T  A  H  Q  Q  P  S  T  A  T  E  E  S  E  L  C  S  T  C  E  F  R  Q
141  ACACAGCAAG CTGATGAGAC TGCATGCCAT CAAGTCCCAA ATTCTTAGCA AACTCCGACT CAAGCAGGCT
       H  S  K  L  M  R  L  H  A  I  K  S  Q  I  L  S  K  L  R  L  K  Q  A
211  CCAAACATCA GCCGGGACGT GGTCAAGCAG CTGTTACCCA AAGCACCGCC TTTGCAACAA CTTCTGGATC
      P  N  I  S  R  D  V  V  K  Q  L  L  P  K  A  P  P  L  Q  Q  L  L  D
281  AGTACGATGT TTTAGGAGAT GACAGTAAGG ATGGAGCTGT GGAAGAGGAC GATGAACATG CCACCACAGA
     Q  Y  D  V  L  G  D  D  S  K  D  G  A  V  E  E  D  D  E  H  A  T  T  E
351  GACCATCATG ACCATGGCCA CAGAACCTGA CCCCATTGTT CAAGTAGATC GGAAACCGAA GTGTTGCTTT
       T  I  M  T  M  A  T  E  P  D  P  I  V  Q  V  D  R  K  P  K  C  C  F
421  TTCTCCTTCA GTCCGAAGAT CCAAGCGAAC CGGATCGTAA GAGCGCAGCT CTGGGTTCAT CTGAGACCGG
      F  S  F  S  P  K  I  Q  A  N  R  I  V  R  A  Q  L  W  V  H  L  R  P
491  CGGAGGAGGC GACCACCGTC TTCTTACAGA TATCTCGGCT GATGCCCGTT AAGGACGGAG GAAGACACCG
     A  E  E  A  T  T  V  F  L  Q  I  S  R  L  M  P  V  K  D  G  G  R  H  R
```

FIG. 2E-1

```
561   AATACGATCC CTGAAAATCG ACGTGAACGC AGGAGTCACG TCTTGGCAGA GTATAGACGT AAAGCAGGTG
        I  R  S   L  K  I  D   V  N  A   G  V  T   S  W  Q  S   I  D  V   K  Q  V
631   CTCACGGTGT GGTTAAAACA ACCGGAGACC AACCGAGGCA TCGAGATTAA CGCATATGAC GCGAAGGGAA
       L  T  V  W   L  K  Q   P  E  T   N  R  G  I   E  I  N   A  Y  D   A  K  G
701   ACGACTTGGC CGTCACTTCA ACCGAGACTG GGGAGGATGG ACTGCTCCCC TTTATGGAGG TGAAAATATC
      N  D  L  A   V  T  S   T  E  T  G   E  D  G   L  L  P   F  M  E  V   K  I  S
771   AGAGGGCCCA AAACGAATCC GGAGGGACTC CGGACTGGAC TGCGATGAGA ATTCCTCAGA GTCTCGCTGC
        E  G  P   K  R  I  R   R  D  S   G  L  D   C  D  E  N   S  S  E   S  R  C
841   TGCAGGTACC CTCTCACTGT GGACTTCGAG GACTTTGGCT GGGACTGGAT TATTGCTCCA AAACGCTATA
       C  R  Y  P   L  T  V   D  F  E   D  F  G  W   D  W  I   I  A  P   K  R  Y
911   AGGCGAATTA CTGTTCAGGA GAATGCGACT ACATGTACCT GCAGAAGTAT CCCCACACCC ATCTGGTGAA
      K  A  N  Y   C  S  G   E  C  D  Y   M  Y  L   Q  K  Y   P  H  T  H   L  V  N
981   CAAGGCCAGT CCGAGAGGAA CGGCTGGGCC CTGCTGCACT CCCACCAAGA TGTCTCCCAT CAAGATGCTT
        K  A  S   P  R  G  T   A  G  P   C  C  T   P  T  K  M   S  P  I   N  M  L
1051  TACTTTAACG GCAAAGAGCA GATCATCTAC GGCAAGATCC CTTCGATGGT AGTAGACCGC TGTGGCTGCT
       Y  F  N  G   K  E  Q   I  I  Y   G  K  I  P   S  M  V   V  D  R   C  G  C
1121  CATGA
       S
```

FIG. 2E-2

salmon GDF-8.nucleotide1
[Strand]

```
1     GGCAGCCGGA GACGAATTGG GGGATCGAGA TTAATGCGTT CGACTCGAAG GGAAATGATC TGGCCGTTAC
        Q  P  E   T  N  W   G  I  E  I   N  A  F   D  S  K   G  N  D  L   A  V  T
71    CTCAGCAGAA GCGGGAGAAG GACTGCAACC CTTCATGGAG GTGACGATTT CAGAGGGCCC GAAGCGCTCC
       S  A  E   A  G  E  G   L  Q  P   F  M  E   V  T  I  S   E  G  P   K  R  S
141   AGGAGAGACT CGGGCCTGGA CTGTGACGAG AACTCCCCCG AGTCCCGCTG TTGCCGCTAC CCCCTCACGG
       R  R  D  S   G  L  D   C  D  E   N  S  P  E   S  R  C   C  R  Y   P  L  T
211   TAGACTTTGA AGACTTTGGC TGGGACTGGA TTATTGCCCC CAAGCGCTAC AAGGCCAACT ACTGCTCTGG
      V  D  F  E   D  F  G   W  D  W  I   I  A  P   K  R  Y   K  A  N  Y   C  S  G
281   TGAGTGTGAG TACATGCACC TGCAGAAGTA CCCCCACACC CACCTGGTGA ACAAGGCTAA CCCTCGCGGC
        E  C  E   Y  M  H  L   Q  K  Y   P  H  T   H  L  V  N   K  A  N   P  R  G
351   ACCGCAGGGC CCTGCTGCAC CCCCACCAAG ATGTCCCCCA TCAACATGCT CTACTTCAAC CGCAAAGAGC
       T  A  G  P   C  C  T   P  T  K   M  S  P  I   N  M  L   Y  F  N   R  K  E
421   AGATCATCTA CGGCAAGATC CCCTCCATGG TGGTGGACCG TTGCGGATGC TCGTGA
      Q  I  I  Y   G  K  I   P  S  M  V   V  D  R   C  G  C   S  .
```

FIG. 2F

salmon GDF8.nucleotide2
[Strand]

```
1    GGTTACCTCA ACTGAAGCCG GAGAAGGACT GCAACCCTTC ATGGAGGTGA AGATTTCGGA GGGCCCGAAG
      V  T  S   T  E  A  G   E  G  L   Q  P  F   M  E  V  K   I  S  E   G  P  K
71   CGCTCCAGGA GAGATTCGGG CCTGGACTGT GATGAGAACT CCCCCGAGTC CCGCTGCTGC CGGTACCCCC
      R  S  R  R   D  S  G   L  D  C   D  E  N  S   P  E  S   R  C  C   R  Y  P
141  TCACGGTGGA CTTTGAAGAC TTTGGCTGGG ACTGGATTAT TGCCCCCAAG CGCTACAAGG CCAACTACTG
     L  T  V  D   F  E  D   F  G  W  D   W  I  I   A  P  K   R  Y  K  A   N  Y  C
211  CTCTGGTGAG TGCGAGTACA TGCACCTGCA GAAGTACCCC CACACCCACC TGGTGAACAA GGCTAACCCT
      S  G  E   C  E  Y  M   H  L  Q   K  Y  P   H  T  H  L   V  N  K   A  N  P
281  CGCGGCACCG CGGGGCCCTG CTGCACCCCC ACCAAGATGT CCCCCATCAA CATGCTCTAC TTCAACCGCA
      R  G  T  A   G  P  C   C  T  P   T  K  M  S   P  I  N   M  L  Y   F  N  R
351  AAGAGCAGAT CATCTACGGC AAGATCCCCT CCATGGTGGT GGACCGCTGC GGCTGCTCGT GA
     K  E  Q  I   I  Y  G   K  I  P  S   M  V  V   D  R  C   G  C  S  .
```

FIG. 2G

```
GDF-8        SRRDFGLDCDEHSTESRCCRYPLTVDF-EAFGWD-WIIAPKRYKANYCSGECEFVFLQKYP——
GDF-1        RPRRDAEPVLGGGPGGACRARRLYVSF-REVGWHRWVIAPRGFLANYCQGQCALPVALSGSGGPP
BMP-2        REKRQAKHKQRKRLKSSCKRHPLYVDF-SDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNS——
BMP-4        KRSPKHHSQRARKKNKNCRRHSLYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNS——
Vgr-1        SRGSGSSDYNGSELKTACKKHELYVSF-QDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNA——
CP-1         LRMANVAENSSSDQRQACKKHELYVSF-RDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNA——
BMP-5        SRMSSVGDYNTSEQKQACKKHELYVSF-RDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNA——
BMP-3        EQTLKKARRKQWIEPRNCARRYLKVDF-ADIGWSEWIISPKSFDAYYCSGACQFPMPKSLKPS—
MIS          GPGRAQRSAGATAADGPCALRELSVDL———RAERSVLIPETYQANNCQGVCGWPQSDRNPRY—
Inhibinbα    ALRLLQRPPEEPAAHANCHRVALNISF-QELGWERWIVYPPSFIFHYCHGGCGLHIPPNLSLPV-
InhibinbβA   HRRRRRGLECDGKV-NICCKKQFFVSF-KDIGWNDWIIAPSGYHANYCEGECPSHIAGISGSSL-
InhibinbβB   HRIRKRGLECDGRT-NLCCRQQFFIDF-RLIGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSAS-
TGF-β1       HRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWK-WIHEPKGYHANFCLGPCPYIWSLD———
TGF-β2       KKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWK-WIHEPKGYNANFCAGACPYLWSSD———
TGF-β3       KKRALDTNYCFRNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD———

GDF-8        -HTHLVHQANPRG—————SAGPCCT—PTKMSPINMLYF-NGKEQIIYGKIPAMVVDRCGCS

GDF-1        ALNHAVLRALMHA—AAPGAADLPCCV—PARLSPISVLFF-DNSDNVVLRQYEDMVVDECGCR
BMP-2        -TNHAIVQTLVNS——VNSKIPKACCV—PTELSAISMLYL-DENEKVVLKNYQDMVVEGCGCR
BMP-4        -TNHAIVQTLVNS——VNSSIPKACCV—PTELSAISMLYL-DEYDKVVLKNYQEMVVEGCGCR
Vgr-1        -TNHAIVQTLVHL—MNPEYVPKPCCA—PTKLNAISVLYF-DDNSNVILKKYRNMVVRACGCH
OP-1         -TNHAIVQTLVHF—INPETVPKPCCA—PTQLNAISVLYF-DDSSNVILKKYRNMVVRACGCH
BMP-5        -TNHAIVQTLVHL—MFPDHVPKPCCA—PTKLNAISVLYF-DDSSNVILKKYRNMVVRSCGCH
BMP-3        —NHATIQSIVRA-VGVVPGIPEPCCV—PEKMSSLSILFF-DENKNVVLKVYPNMTVESCACR
MIS          -GNHVVLLLKMQA—RGAALARPPCCV—PTAYAGKLLISLSEER—ISAHHVPNMVATECGCR
Inhibinα     -PGAPPTPAQPYS———LLPGAQPCCAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTCHCACI
InhibinβA    -SFHSTVINHYRMRGHSPFANLKSCCV—PTKLRPMSMLYY-DDGQNIIKKDIQNMIVEECGCS
InhibinβB    -SFHTAVVNQYRMRGLNPGT-VNSCCI—PTKLSTMSMLYF-DDEYNIVKRDVPNMIVEECGCA
TGF-β1       -TQYSKVLALYNQ—HNPGASAAPCCV—PQALEPLPIVYY-VGRKPKV-EQLSNMIVRSCKCS
TGF-β2       -TQHSRVLSLYNT—INPEASASPCCV—SQDLEPLTILYY-IGKTPKI-EQLSNMIVKSCKCS
TGF-β3       -TTHSTVLGLYNT—LNPEASASPCCV—PQDLEPLTILYY-VGRTPKV-EQLSNMVVKSCKCS
```

FIG. 3A

```
        1                                                                              80
  human  MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDVIRQ
 murine MMQKLQMYVYIYLFMLIAAGPVDLNEGSEKEENVEKEGLCNACAWRQNTRYSRIEAIKIQILSKLRLETAPNISKDAIRQ
    rat
chicken

        81                                                                            160
  human LLPKAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDFLMQVDGKPKCCFFKFSSKIQYNKVVKAQLWIY
 murine LLPRAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDFLMQADGKPKCCFFKFSSKIQYNKVVKAQLWIY
    rat
chicken                                                                       LVVKAQLWIY

        161                                                                           240
  human LRPVETPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV
 murine LRPVKTPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMSPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV
    rat
chicken LRQVQKPTTVFVQILRLIKPMKDGTRYTGIGSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKAFDETGRDLAV

        241                                                                           320
  human TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRTPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ
 murine TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ
    rat       EDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ
chicken TFPGPGEDGLNPFLEVRVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ

        321                                                    376
  human KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
 murine KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
    rat KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
chicken KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
```

FIG. 3B

```
                                 10                  20                  30
  1 M M Q K L Q M Y V Y I Y L F M L I A A G P V D L N E G S E R   murine
  1 M H F T Q - - - V L I S L S V L I A C G P V G Y G D I T A H   zebrafish
  1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon1
  1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon2

                                 40                  50                  60
 31 E E - - - N V E K E G L C N A C A W R Q N T R Y S R I E A I   murine
 28 Q Q P S T A T E E S E L C S T C E F R Q H S K L M R L H A I   zebrafish
  1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon1
  1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon2

                                 70                  80                  90
 58 K I Q I L S K L R L E T A P N I S K D A I R Q L L P R A P P   murine
 58 K S Q I L S K L R L K Q A P N I S R D V V K Q L L P K A P P   zebrafish
  1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon1
  1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon2

                                100                 110                 120
 88 L R E L I D Q Y D V Q R D D S S D G S L E D D D Y H A T T E   murine
 88 L Q Q L L D Q Y D V L G D D S K D G A V E E D D E H A T T E   zebrafish
  1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon1
  1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon2

                                130                 140                 150
118 T I I T M P T E S D F L M Q A D G K P K C C F F K F S S K I   murine
118 T I M T M A T E P D P I V Q V D R K P K C C F F S F S P K I   zebrafish
  1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon1
  1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon2
```

FIG. 3C

```
                                  160                                     170                                     180
148  Q Y N K V V K A Q L W I Y L R P V K T P T T V F V Q I L R L   murine
148  Q A N R I V R A Q L W V H L R P A E E A T T V F L Q I S R L   zebrafish
  1  - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon1
  1  - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon2

                                  190                                     200                                     210
178  I K P M K D G T R Y T G I R S L K L D M S P G T G I W Q S I   murine
178  M - P V K D G G R H R - I R S L K I D V N A G V T S W Q S I   zebrafish
  1  - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon1
  1  - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon2

                                  220                                     230                                     240
208  D V K T V L Q N W L K Q P E S N L G I E I K A L D E N G H D   murine
206  D V K Q V L T V W L K Q P E T N R G I E I N A Y D A K G N D   zebrafish
  1  - - - - - - - - - - - Q P E T N W G I E I N A F D S K G N D   salmon1
  1  - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   salmon2

                                  250                                     260                                     270
238  L A V T F P G P G E D G L N P F L E V K V T D T P K R S R R   murine
236  L A V T S T E T G E D G L L P F M E V K I S E G P K R I R R   zebrafish
 20  L A V T S A E A G E - G L Q P F M E V T I S E G P K R S R R   salmon1
  1  - - V T S T E A G E - G L Q P F M E V K I S E G P K R S R R   salmon2

                                  280                                     290                                     300
268  D F G L D C D E H S T E S R C C R Y P L T V D F E A F G W D   murine
266  D S G L D C D E N S S E S R C C R Y P L T V D F E D F G W D   zebrafish
 49  D S G L D C D E N S P E S R C C R Y P L T V D F E D F G W D   salmon1
 28  D S G L D C D E N S P E S R C C R Y P L T V D F E D F G W D   salmon2
```

FIG. 3D

```
                                   310                 320                 330
298 W I I A P K R Y K A N Y C S G E C E F V F L Q K Y P H T H L  murine
296 W I I A P K R Y K A N Y C S G E C D Y M Y L Q K Y P H T H L  zebrafish
 79 W I I A P K R Y K A N Y C S G E C E Y M H L Q K Y P H T H L  salmon1
 58 W I I A P K R Y K A N Y C S G E C E Y M H L Q K Y P H T H L  salmon2

                                   340                 350                 360
328 V H Q A N P R G S A G P C C T P T K M S P I N M L Y F N G K  murine
326 V N K A S P R G T A G P C C T P T K M S P I N M L Y F N G K  zebrafish
109 V N K A N P R G T A G P C C T P T K M S P I N M L Y F N R K  salmon1
 88 V N K A N P R G T A G P C C T P T K M S P I N M L Y F N R K  salmon2

                                   370
358 E Q I I Y G K I P A M V V D R C G C S  murine
356 E Q I I Y G K I P S M V V D R C G C S  zebrafish
139 E Q I I Y G K I P S M V V D R C G C S  salmon1
118 E Q I I Y G K I P S M V V D R C G C S  salmon2
```

Decoration 'Decoration #1': The outlined residues that match the Concensus exactly.

FIG. 3E

	GDF-1	GDF-2	GDF-3	GDF-5	GDF-6	GDF-7	GDF-8	GDF-9	BMP-2	BMP-4	Vgr-1	OP-1	BMP-5	BMP-3	MIS	Inhibinα	InhibinβA	InhibinβB	TGF-β1	TGF-β2	TGF-β3
GDF-1	100	33	50	46	44	48	35	27	42	43	46	47	46	42	34	23	37	35	33	32	33
GDF-2	-	100	42	47	51	48	31	32	52	51	55	52	55	34	20	20	32	25	26	28	30
GDF-3	-	-	100	49	49	46	41	33	53	50	53	50	50	42	22	25	42	41	36	31	32
GDF-5	-	-	-	100	86	80	37	33	57	57	51	51	52	47	27	24	40	37	33	34	37
GDF-6	-	-	-	-	100	80	38	34	57	56	53	53	54	46	26	27	43	39	35	36	38
GDF-7	-	-	-	-	-	100	37	33	57	57	52	53	52	46	25	26	41	36	36	35	38
GDF-8	-	-	-	-	-	-	100	27	41	38	45	42	42	38	31	26	38	42	34	37	37
GDF-9	-	-	-	-	-	-	-	100	33	34	31	30	31	29	21	27	30	31	23	25	25
BMP-2	-	-	-	-	-	-	-	-	100	92	61	60	61	48	27	22	42	42	35	34	36
BMP-4	-	-	-	-	-	-	-	-	-	100	60	58	59	47	27	22	41	42	34	33	35
Vgr-1	-	-	-	-	-	-	-	-	-	-	100	87	91	44	24	25	44	41	35	37	39
OP-1	-	-	-	-	-	-	-	-	-	-	-	100	88	42	27	24	43	42	34	38	38
BMP-5	-	-	-	-	-	-	-	-	-	-	-	-	100	43	24	24	43	37	34	35	36
BMP-3	-	-	-	-	-	-	-	-	-	-	-	-	-	100	30	29	36	37	32	32	32
MIS	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	18	24	25	28	23	25
Inhibinα	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	26	25	23	22	24
InhibinβA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	63	41	37	36
InhibinβB	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	35	34	37
TGG-β1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	74	78
TGF-β2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	82
TGF-β3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100

FIG. 4

```
   1 GTCTCTCGGACGGTACATGCACTAATATTTCACTTGGCATTACTCAAAAGCAAAAAGAAG 60
  61 AAATAAGAACAAGGGAAAAAAAAAGATTGTGCTGATTTTTAAAATGATGCAAAAACTGCA 120
                                                M  M  Q  K  L  Q
 121 AATGTATGTTTATATTTACCTGTTCATGCTGATTGCTGCTGGCCCAGTGGATCTAAATGA 180
      M  Y  V  Y  I  Y  L  F  M  L  I  A  A  G  P  V  D  L  N  E
 181 GGGCAGTGAGAGAGAAGAAAATGTGGAAAAAGAGGGGCTGTGTAATGCATGTGCGTGGAG 240
      G  S  E  R  E  E  N  V  E  K  E  G  L  C  N  A  C  A  W  R
 241 ACAAAACACGAGGTACTCCAGAATAGAAGCCATAAAAATTCAAATCCTCAGTAAGCTGCG 300
      Q  N  T  R  Y  S  R  I  E  A  I  K  I  Q  I  L  S  K  L  R
 301 CCTGGAAACAGCTCCTAACATCAGCAAAGATGCTATAAGACAACTTCTGCCAAGAGCGCC 360
      L  E  T  A  P [N  I  S] K  D  A  I  R  Q  L  L  P  R  A  P
 361 TCCACTCCGGGAACTGATCGATCAGTACGACGTCCAGAGGGATGACAGCAGTGATGGCTC 420
      P  L  R  E  L  I  D  Q  Y  D  V  Q  R  D  D  S  S  D  G  S
 421 TTTGGAAGATGACGATTATCACGCTACCACGGAAACAATCATTACCATGCCTACAGAGTC 480
      L  E  D  D  D  Y  H  A  T  T  E  T  I  I  T  M  P  T  E  S
 481 TGACTTTCTAATGCAAGCGGATGGCAAGCCCAAATGTTGCTTTTTTAAATTTAGCTCTAA 540
      D  F  L  M  Q  A  D  G  K  P  K  C  C  F  F  K  F  S  S  K
 541 AATACAGTACAACAAAGTAGTAAAAGCCCAACTGTGGATATATCTCAGACCCGTCAAGAC 600
      I  Q  Y  N  K  V  V  K  A  Q  L  W  I  Y  L  R  P  V  K  T
 601 TCCTACAACAGTGTTTGTGCAAATCCTGAGACTCATCAAACCCATGAAAGACGGTACAAG 660
      P  T  T  V  F  V  Q  I  L  R  L  I  K  P  M  K  D  G  T  R
 661 GTATACTGGAATCCGATCTCTGAAACTTGACATGAGCCCAGGCACTGGTATTTGGCAGAG 720
      Y  T  G  I  R  S  L  K  L  D  M  S  P  G  T  G  I  W  Q  S
 721 TATTGATGTGAAGACAGTGTTGCAAAATTGGCTCAAACAGCCTGAATCCAACTTAGGCAT 780
      I  D  V  K  T  V  L  Q  N  W  L  K  Q  P  E  S  N  L  G  I
 781 TGAAATCAAAGCTTTGGATGAGAATGGCCATGATCTTGCTGTAACCTTCCCAGGACCAGG 840
      E  I  K  A  L  D  E  N  G  H  D  L  A  V  T  F  P  G  P  G
 841 AGAAGATGGGCTGAATCCCTTTTTAGAAGTCAAGGTGACAGACACACCCAAGAGGTCCCG 900
      E  D  G  L  N  P  F  L  E  V  K  V  T  D  T  P  K [R  S  R
 901 GAGAGACTTTGGGCTTGACTGCGATGAGCACTCCACGGAATCCCGGTGCTGCCGCTACCC 960
      R] D  F  G  L  D  C  D  E  H  S  T  E  S  R  C  C  R  Y  P
 961 CCTCACGGTCGATTTTGAAGCCTTTGGATGGGACTGGATTATCGCACCCAAAAGATATAA 1020
      L  T  V  D  F  E  A  F  G  W  D  W  I  I  A  P  K  R  Y  K
1021 GGCCAATTACTGCTCAGGAGAGTGTGAATTTGTGTTTTTACAAAAATATCCGCATACTCA 1080
      A  N  Y  C  S  G  E  C  E  F  V  F  L  Q  K  Y  P  H  T  H
1081 TCTTGTGCACCAAGCAAACCCCAGAGGCTCAGCAGGCCCTTGCTGCACTCCGACAAAAAT 1140
      L  V  H  Q  A  N  P  R  G  S  A  G  P  C  C  T  P  T  K  M
1141 GTCTCCCATTAATATGCTATATTTTAATGGCAAAGAACAAATAATATATGGAAAAATTCC 1200
      S  P  I  N  M  L  Y  F  N  G  K  E  Q  I  I  Y  G  K  I  P
1201 AGCCATGGTAGTAGACCGCTGTGGGTGCTCATGAGCTTTGCATTAGGTTAGAAACTTCCC 1260
      A  M  V  V  D  R  C  G  C  S  *
```

FIG. 5A

1261 AAGTCATGGAAGGTCTTCCCCTCAATTTCGAAACTGTGAATTCAAGCACCACAGGCTGTA 1320
1321 GGCCTTGAGTATGCTCTAGTAACGTAAGCACAAGCTACAGTGTATGAACTAAAAGAGAGA 1380
1381 ATAGATGCAATGGTTGGCATTCAACCACCAAAATAAACCATACTATAGGATGTTGTATGA 1440
1441 TTTCCAGAGTTTTTGAAATAGATGGAGATCAAATTACATTTATGTCCATATATGTATATT 1500
1501 ACAACTACAATCTAGGCAAGGAAGTGAGAGCACATCTTGTGGTCTGCTGAGTTAGGAGGG 1560
1561 TATGATTAAAAGGTAAAGTCTTATTTCCTAACAGTTTCACTTAATATTTACAGAAGAATC 1620
1621 TATATGTAGCCTTTGTAAAGTGTAGGATTGTTATCATTTAAAAACATCATGTACACTTAT 1680
1681 ATTTGTATTGTATACTTGGTAAGATAAAATTCCACAAAGTAGGAATGGGGCCTCACATAC 1740
1741 ACATTGCCATTCCTATTATAATTGGACAATCCACCACGGTGCTAATGCAGTGCTGAATGG 1800
1801 CTCCTACTGGACCTCTCGATAGAACACTCTACAAAGTACGAGTCTCTCTCTCCCTTCCAG 1860
1861 GTGCATCTCCACACACACAGCACTAAGTGTTCAATGCATTTTCTTTAAGGAAAGAAGAAT 1920
1921 CTTTTTTTCTAGAGGTCAACTTTCAGTCAACTCTAGCACAGCGGGAGTGACTGCTGCATC 1980
1981 TTAAAAGGCAGCCAAACAGTATTCATTTTTTAATCTAAATTTCAAAATCACTGTCTGCCT 2040
2041 TTATCACATGGCAATTTTGTGGTAAAATAATGGAAATGACTGGTTCTATCAATATTGTAT 2100
2101 AAAAGACTCTGAAACAATTACATTTATATAATATGTATACAATATTGTTTTGTAAATAAG 2160
2161 TGTCTCCTTTTATATTTACTTTGGTATATTTTTACACTAATGAAATTTCAAATCATTAAA 2220
2221 GTACAAAGACATGTCATGTATCACAAAAAAGGTGACTGCTTCTATTTCAGAGTGAATTAG 2280
2281 CAGATTCAATAGTGGTCTTAAAACTCTGTATGTTAAGATTAGAAGGTTATATTACAATCA 2340
2341 ATTTATGTATTTTTTACATTATCAACTTATGGTTTCATGGTGGCTGTATCTATGAATGTG 2400
2401 GCTCCCAGTCAAATTTCAATGCCCCACCATTTTAAAAATTACAAGCATTACTAAACATAC 2460
2461 CAACATGTATCTAAAGAAATACAAATATGGTATCTCAATAACAGCTACTTTTTTATTTTA 2520
2521 TAATTTGACAATGAATACATTTCTTTTATTTACTTCAGTTTTATAAATTGGAACTTTGTT 2580
2581 TATCAAATGTATTGTACTCATAGCTAAATGAAATTATTTCTTACATAAAAATGTGTAGAA 2640
2641 ACTATAAATTAAAGTGTTTTCACATTTTGAAAGGC 2676

FIG. 5B

```
   1 AAGAAAAGTAAAAGGAAGAAACAAGAACAAGAAAAAAGATTATATTGATTTTAAAATCAT 60
                                                                M
  61 GCAAAAACTGCAACTCTGTGTTTATATTTACCTGTTTATGCTGATTGTTGCTGGTCCAGT 120
       Q  K  L  Q  L  C  V  Y  I  Y  L  F  M  L  I  V  A  G  P  V
 121 GGATCTAAATGAGAACAGTGAGCAAAAAGAAAATGTGGAAAAAGAGGGGCTGTGTAATGC 180
       D  L  N  E  N  S  E  Q  K  E  N  V  E  K  E  G  L  C  N  A
 181 ATGTACTTGGAGACAAAACACTAAATCTTCAAGAATAGAAGCCATTAAGATACAAATCCT 240
       C  T  W  R  Q  N  T  K  S  S  R  I  E  A  I  K  I  Q  I  L
 241 CAGTAAACTTCGTCTGGAAACAGCTCCTAACATCAGCAAAGATGTTATAAGACAACTTTT 300
       S  K  L  R  L  E  T  A  P  N  I  S  K  D  V  I  R  Q  L  L
 301 ACCCAAAGCTCCTCCACTCCGGGAACTGATTGATCAGTATGATGTCCAGAGGGATGACAG 360
       P  K  A  P  P  L  R  E  L  I  D  Q  Y  D  V  Q  R  D  D  S
 361 CAGCGATGGCTCTTTGGAAGATGACGATTATCACGCTACAACGGAAACAATCATTACCAT 420
       S  D  G  S  L  E  D  D  D  Y  H  A  T  T  E  T  I  I  T  M
 421 GCCTACAGAGTCTGATTTTCTAATGCAAGTGGATGGAAAACCCAAATGTTGCTTCTTTAA 480
       P  T  E  S  D  F  L  M  Q  V  D  G  K  P  K  C  C  F  F  K
 481 ATTTAGCTCTAAAATACAATACAATAAAGTAGTAAAGGCCCAACTATGGATATATTTGAG 540
       F  S  S  K  I  Q  Y  N  K  V  V  K  A  Q  L  W  I  Y  L  R
 541 ACCCGTCGAGACTCCTACAACAGTGTTTGTGCAAATCCTGAGACTCATCAAACCTATGAA 600
       P  V  E  T  P  T  T  V  F  V  Q  I  L  R  L  I  K  P  M  K
 601 AGACGGTACAAGGTATACTGGAATCCGATCTCTGAAACTTGACATGAACCCAGGCACTGG 660
       D  G  T  R  Y  T  G  I  R  S  L  K  L  D  M  N  P  G  T  G
 661 TATTTGGCAGAGCATTGATGTGAAGACAGTGTTGCAAAATTGGCTCAAACAACCTGAATC 720
       I  W  Q  S  I  D  V  K  T  V  L  Q  N  W  L  K  Q  P  E  S
 721 CAACTTAGGCATTGAAATAAAAGCTTTAGATGAGAATGGTCATGATCTTGCTGTAACCTT 780
       N  L  G  I  E  I  K  A  L  D  E  N  G  H  D  L  A  V  T  F
 781 CCCAGGACCAGGAGAAGATGGGCTGAATCCGTTTTTAGAGGTCAAGGTAACAGACACACC 840
       P  G  P  G  E  D  G  L  N  P  F  L  E  V  K  V  T  D  T  P
 841 AAAAAGATCCAGAAGGGATTTTGGTCTTGACTGTGATGAGCACTCAACAGAATCACGATG 900
       K  R  S  R  R  D  F  G  L  D  C  D  E  H  S  T  E  S  R  C
 901 CTGTCGTTACCCTCTAACTGTGGATTTTGAAGCTTTTGGATGGGATTGGATTATCGCTCC 960
       C  R  Y  P  L  T  V  D  F  E  A  F  G  W  D  W  I  I  A  P
 961 TAAAAGATATAAGGCCAATTACTGCTCTGGAGAGTGTGAATTTGTATTTTTACAAAAATA 1020
       K  R  Y  K  A  N  Y  C  S  G  E  C  E  F  V  F  L  Q  K  Y
1021 TCCTCATACTCATCTGGTACACCAAGCAAACCCCAGAGGTTCAGCAGGCCCTTGCTGTAC 1080
       P  H  T  H  L  V  H  Q  A  N  P  R  G  S  A  G  P  C  C  T
1081 TCCCACAAAGATGTCTCCAATTAATATGCTATATTTTAATGGCAAAGAACAAATAATATA 1140
       P  T  K  M  S  P  I  N  M  L  Y  F  N  G  K  E  Q  I  I  Y
1141 TGGGAAAATTCCAGCGATGGTAGTAGACCGCTGTGGGTGCTCATGAGATTTATATTAAGC 1200
       G  K  I  P  A  M  V  V  D  R  C  G  C  S  *
```

FIG. 5C

1201 GTTCATAACTTCCTAAAACATGGAAGGTTTTCCCCTCAACAATTTTGAAGCTGTGAAATT 1260
1261 AAGTACCACAGGCTATAGGCCTAGAGTATGCTACAGTCACTTAAGCATAAGCTACAGTAT 1320
1321 GTAAACTAAAAGGGGGAATATATGCAATGGTTGGCATTTAACCATCCAAACAAATCATAC 1380
1381 AAGAAAGTTTTATGATTTCCAGAGTTTTTGAGCTAGAAGGAGATCAAATTACATTTATGT 1440
1441 TCCTATATATTACAACATCGGCGAGGAAATGAAAGCGATTCTCCTTGAGTTCTGATGAAT 1500
1501 TAAAGGAGTATGCTTTAAAGTCTATTTCTTTAAAGTTTTGTTTAATATTTACAGAAAAAT 1560
1561 CCACATACAGTATTGGTAAAATGCAGGATTGTTATATACCATCATTCGAATCATCCTTAA 1620
1621 ACACTTGAATTTATATTGTATGGTAGTATACTTGGTAAGATAAAATTCCACAAAAATAGG 168C
1681 GATGGTGCAGCATATGCAATTTCCATTCCTATTATAATTGACACAGTACATTAACAATCC 1740
1741 ATGCCAACGGTGCTAATACGATAGGCTGAATGTCTGAGGCTACCAGGTTTATCACATAAA 1800
1801 AAACATTCAGTAAAATAGTAAGTTTCTCTTTTCTTCAGGTGCATTTTCCTACACCTCCAA 1860
1861 ATGAGGAATGGATTTTCTTTAATGTAAGAAGAATCATTTTTCTAGAGGTTGGCTTTCAAT 1920
1921 TCTGTAGCATACTTGGAGAAACTGCATTATCTTAAAAGGCAGTCAAATGGTGTTTGTTTT 1980
1981 TATCAAAATGTCAAAATAACATACTTGGAGAAGTATGTAATTTTGTCTTTGGAAAATTAC 2040
2041 AACACTGCCTTTGCAACACTGCAGTTTTTATGGTAAAATAATAGAAATGATCGACTCTAT 2100
2101 CAATATTGTATAAAAAGACTGAAACAATGCATTTATATAATATGTATACAATATTGTTTT 2160
2161 GTAAATAAGTGTCTCCTTTTTTATTTACTTTGGTATATTTTTACACTAAGGACATTTCAA 2220
2221 ATTAAGTACTAAGGCACAAAGACATGTCATGCATCACAGAAAAGCAACTACTTATATTTC 2280
2281 AGAGCAAATTAGCAGATTAAATAGTGGTCTTAAAACTCCATATGTTAATGATTAGATGGT 2340
2341 TATATTACAATCATTTTATATTTTTTTACATGATTAACATTCACTTATGGATTCATGATG 2400
2401 GCTGTATAAAGTGAATTTGAAATTTCAATGGTTTACTGTCATTGTGTTTAAATCTCAACG 2460
2461 TTCCATTATTTTAATACTTGCAAAAACATTACTAAGTATACCAAAATAATTGACTCTATT 2520
2521 ATCTGAAATGAAGAATAAACTGATGCTATCTCAACAATAACTGTTACTTTTATTTTATAA 2580
2581 TTTGATAATGAATATATTTCTGCATTTATTTACTTCTGTTTTGTAAATTGGGATTTTGTT 2640
2641 AATCAAATTTATTGTACTATGACTAAATGAAATTATTTCTTACATCTAATTTGTAGAAAC 2700
2701 AGTATAAGTTATATTAAAGTGTTTTCACATTTTTTTGAAAGAC 2743

FIG. 5D

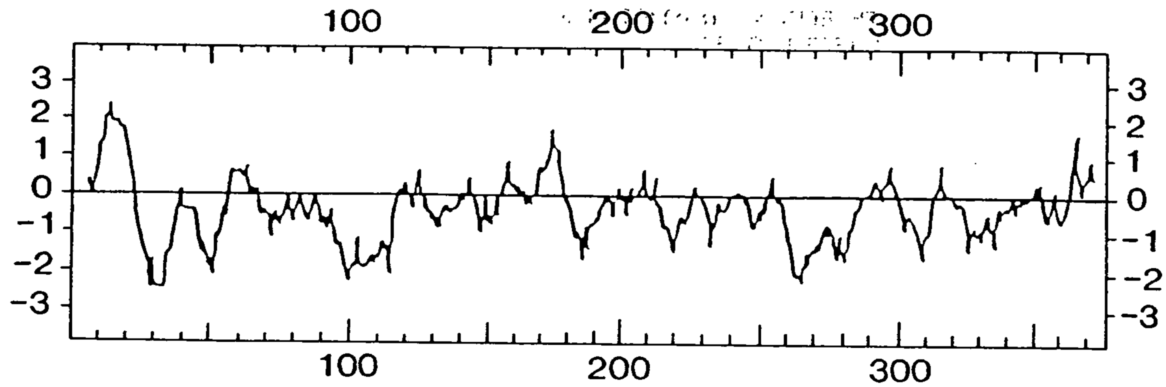


FIG. 6A

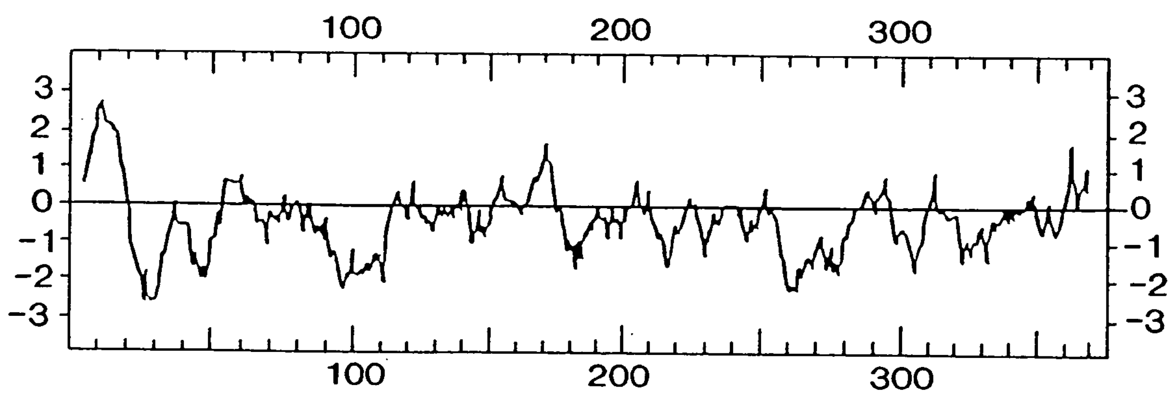


FIG. 6B

```
1    MMQKLQMYVYIYLFMLIAAGPVDLNEGSEREENVEKEGLCNACAWRQNTR   50
1     MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTK   49

51   YSRIEAIKIQILSKLRLETAPNISKDAIRQLLPRAPPLRELIDQYDVQRD   100
50   SSRIEAIKIQILSKLRLETAPNISKDVIRQLLPKAPPLRELIDQYDVQRD   99

101  DSSDGSLEDDDYHATTETIITMPTESDFLMQADGKPKCCFFKFSSKIQYN   150
100  DSSDGSLEDDDYHATTETIITMPTESDFLMQVDGKPKCCFFKFSSKIQYN   149

151  KVVKAQLWIYLRPVKTPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMSPG   200
150  KVVKAQLWIYLRPVETPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPG   199

201  TGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAVTFPGPGEDGL   250
200  TGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAVTFPGPGEDGL   249

251  NPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWII   300
250  NPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWII   299

301  APKRYKANYCSGECEFVFLQKYPHTHLVHQANPRGSAGPCCTPTKMSPIN   350
300  APKRYKANYCSGECEFVFLQKYPHTHLVHQANPRGSAGPCCTPTKMSPIN   349

351  MLYFNGKEQIIYGKIPAMVVDRCGCS   376
350  MLYFNGKEQIIYGKIPAMVVDRCGCS   375
```

FIG. 7

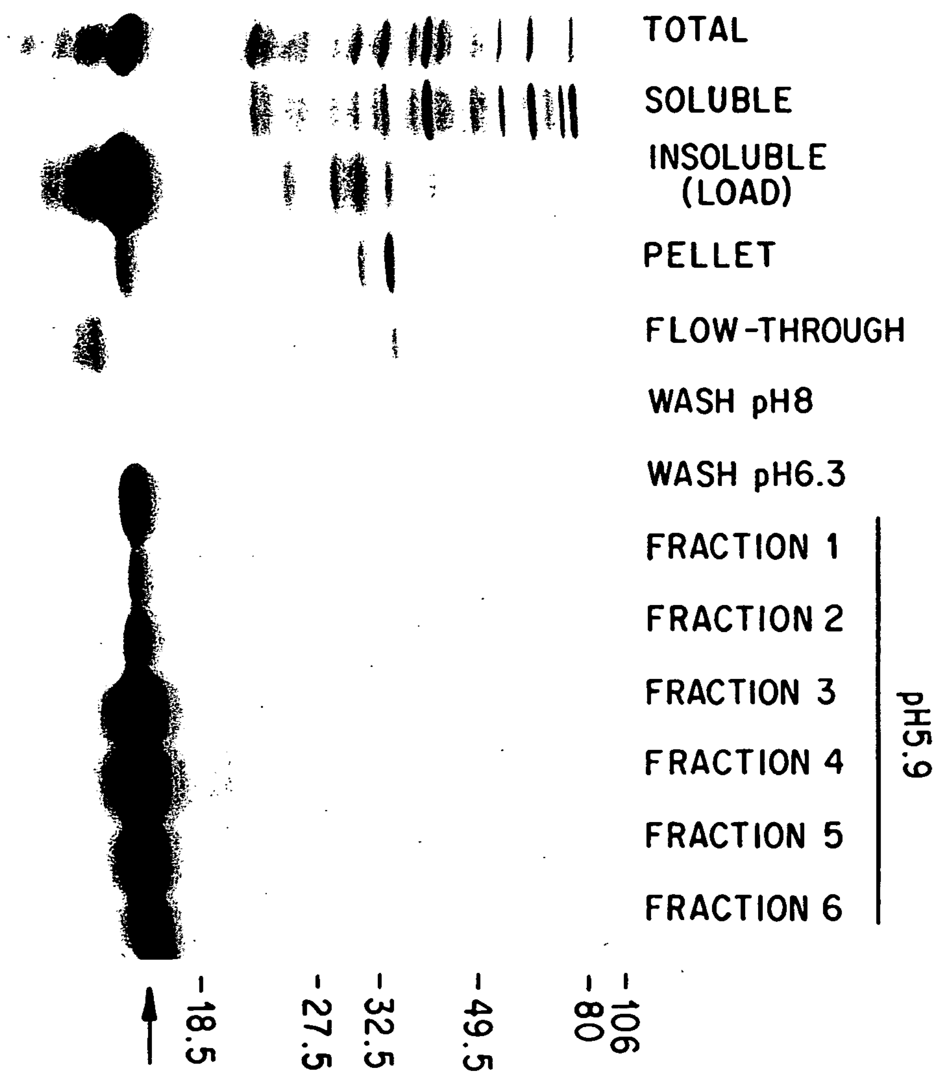

TOTAL
SOLUBLE
INSOLUBLE (LOAD)
PELLET
FLOW-THROUGH
WASH pH8
WASH pH6.3
FRACTION 1
FRACTION 2
FRACTION 3
FRACTION 4
FRACTION 5
FRACTION 6
pH5.9
-18.5
-27.5
-32.5
-49.5
-80
-106

FIG. 8

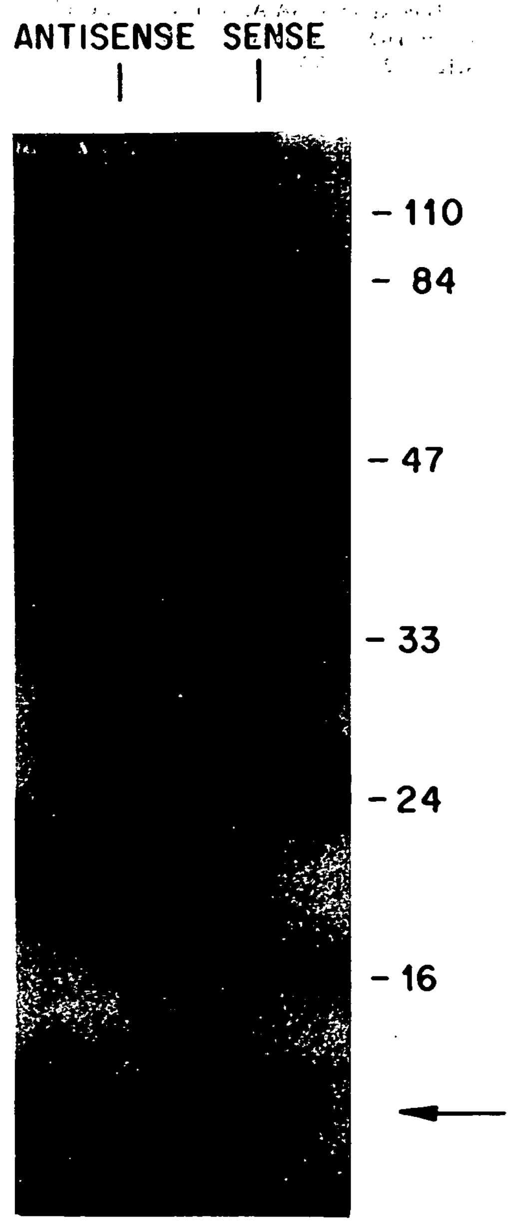
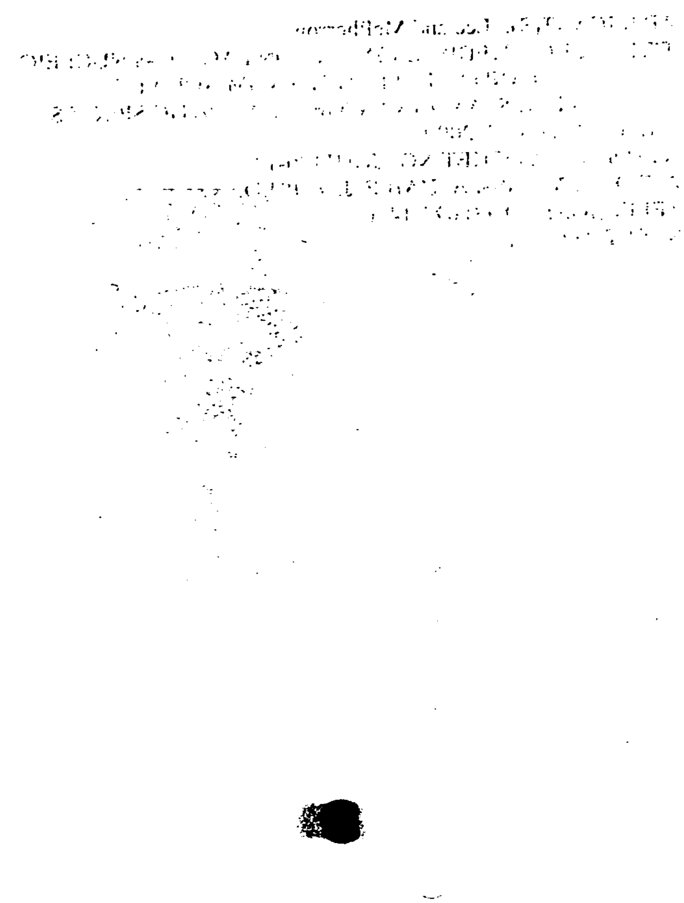


FIG. 9



HEART
LUNG
THYMUS
BRAIN
KIDNEY
SEMINAL VESICLE
PANCREAS
INTESTINE
SPLEEN
TESTIS
MUSCLE
LIVER
OVARY
FAT
UTERUS

—2.9 kb

FIG. 10a

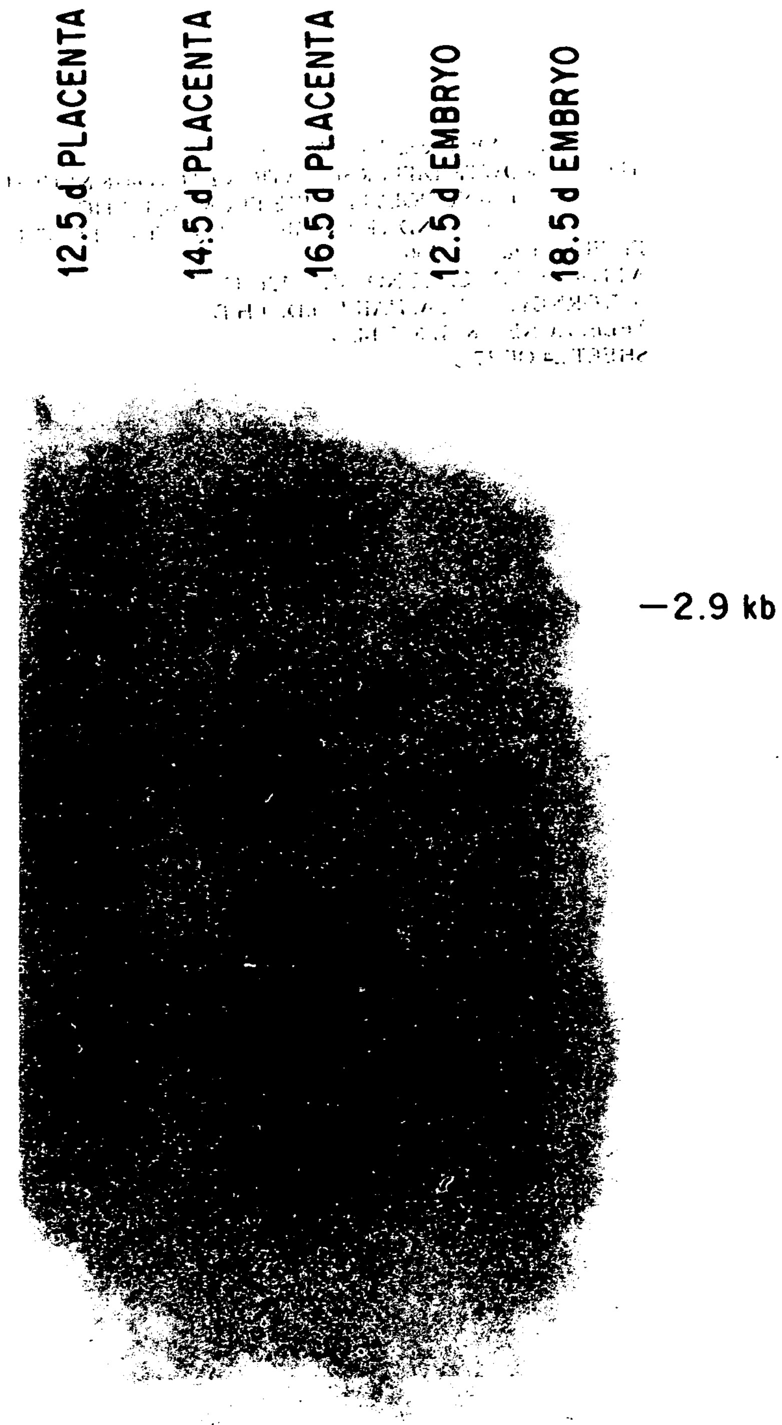

12.5 d PLACENTA
14.5 d PLACENTA
16.5 d PLACENTA
12.5 d EMBRYO
18.5 d EMBRYO
—2.9 kb

FIG. 10b

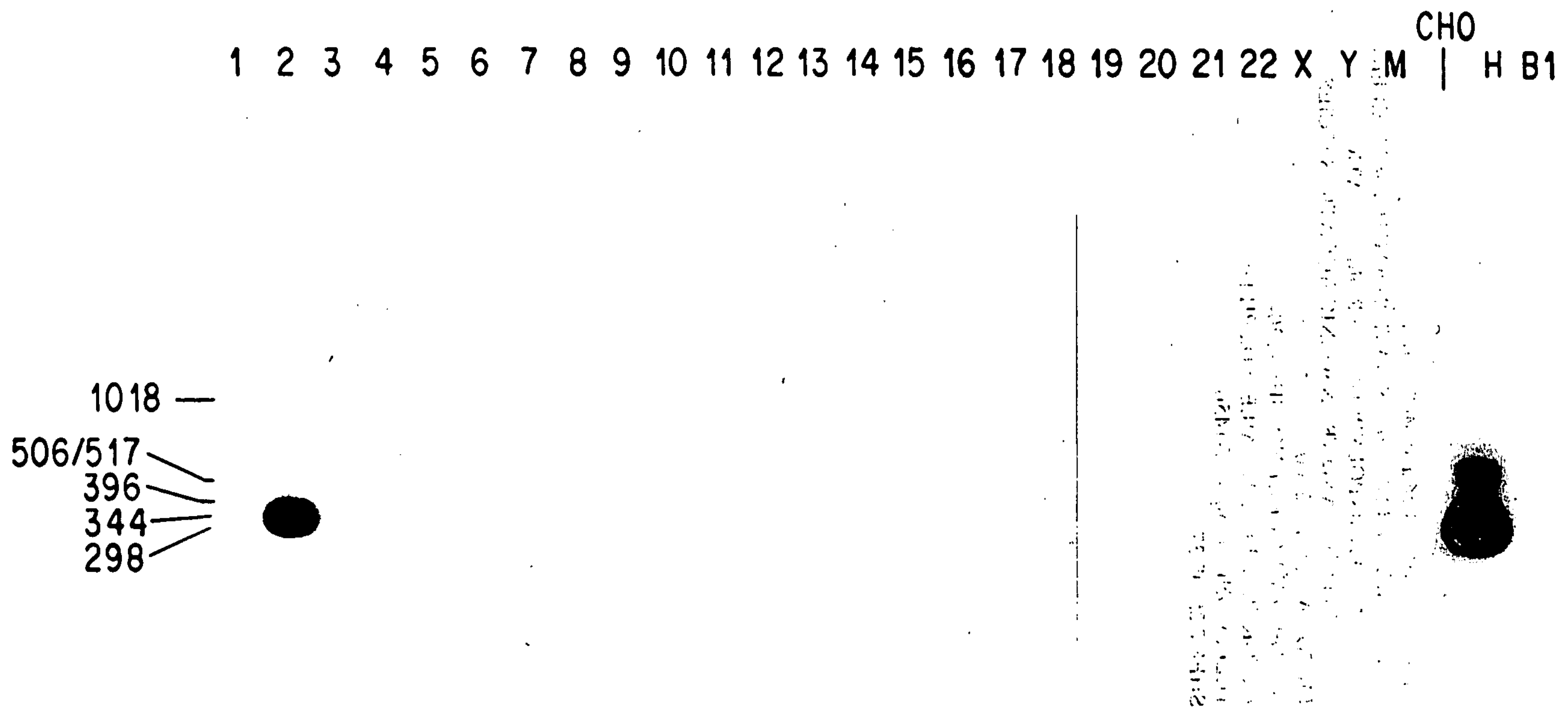

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y M CHO H B1
1018
506/517
396
344
298

FIG. 11

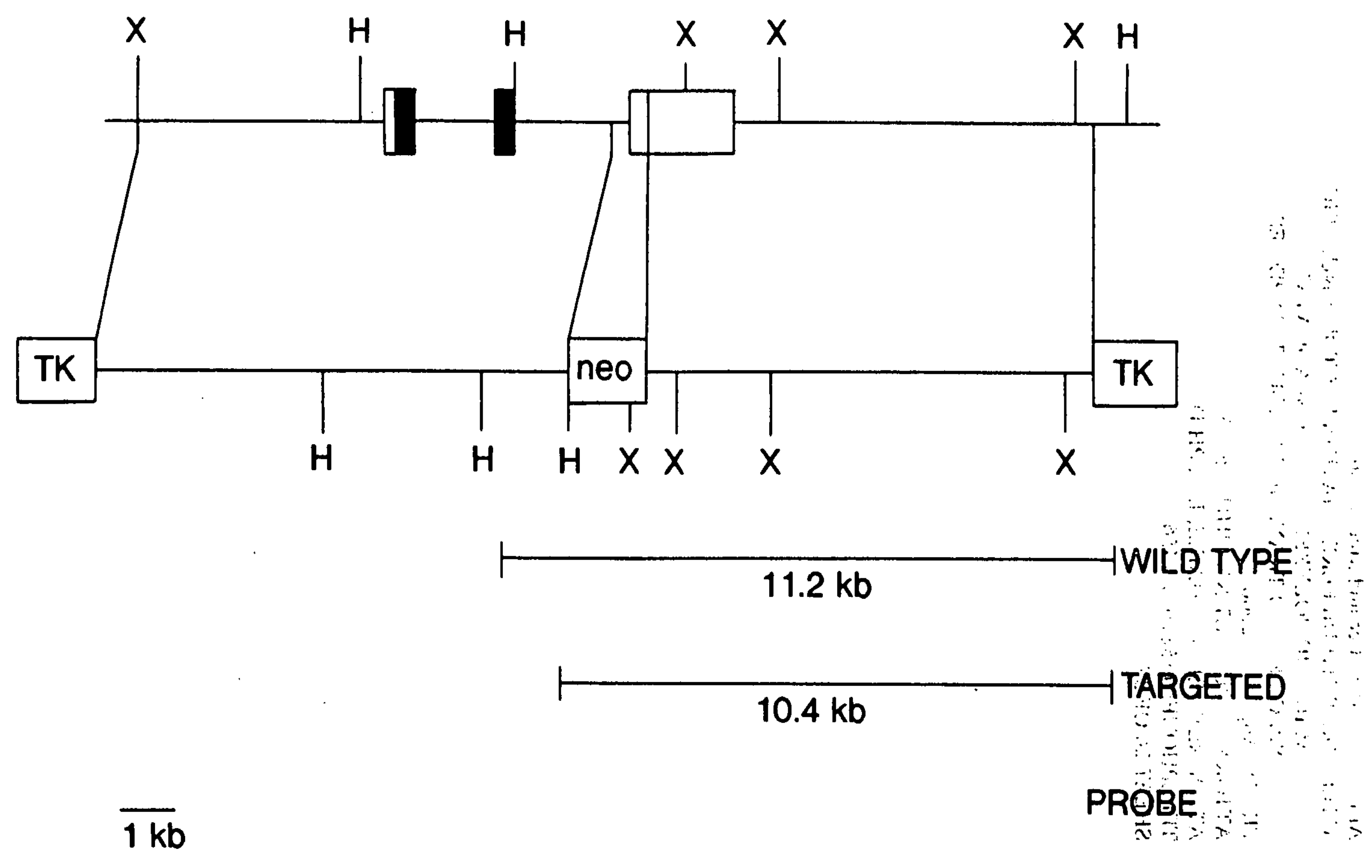

X
H
H
X
X
X
H
TK
neo
TK
H
H
H
X
X
X
X
WILD TYPE
11.2 kb
TARGETED
10.4 kb
PROBE
1 kb

FIG. 12A

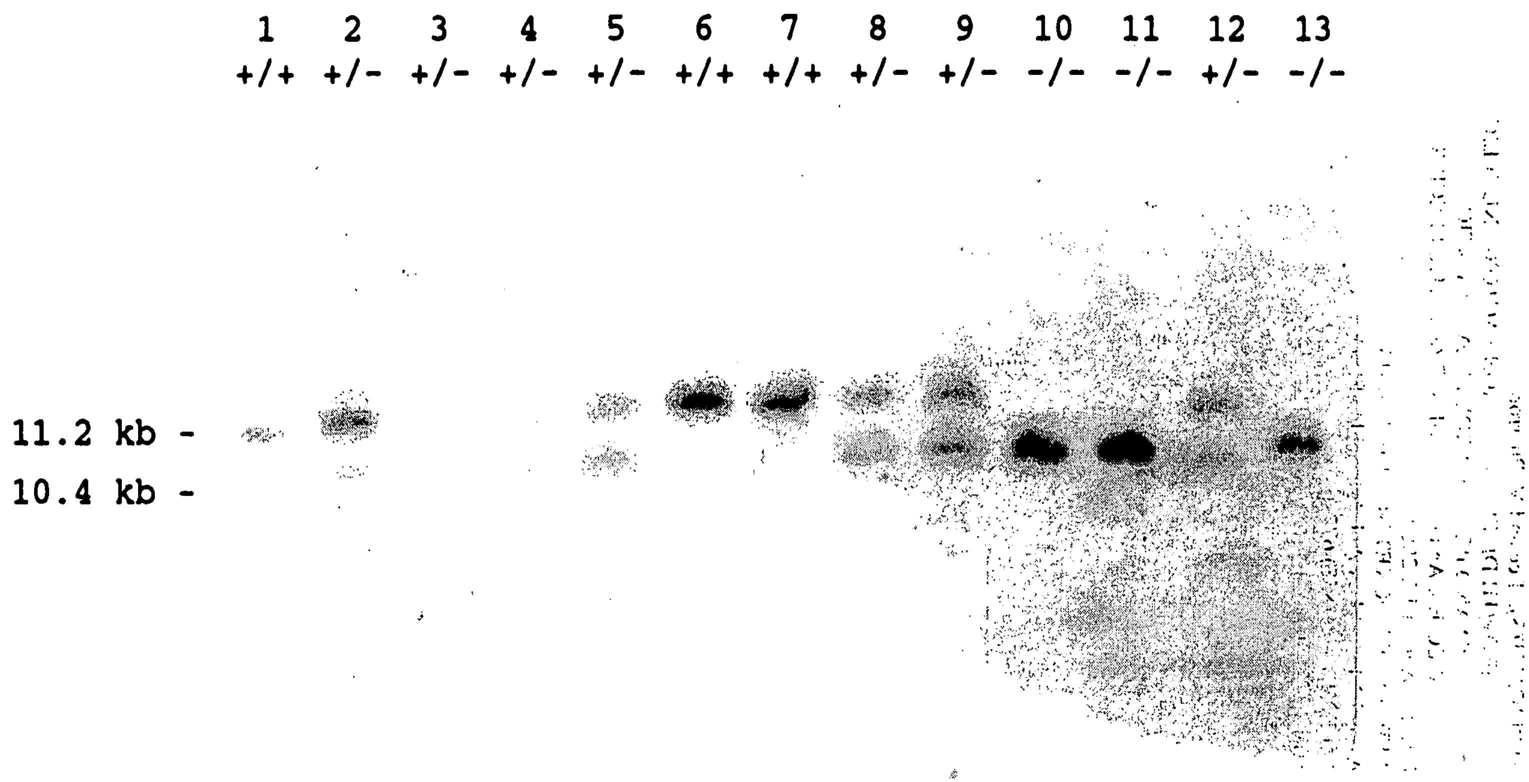


FIG. 12b

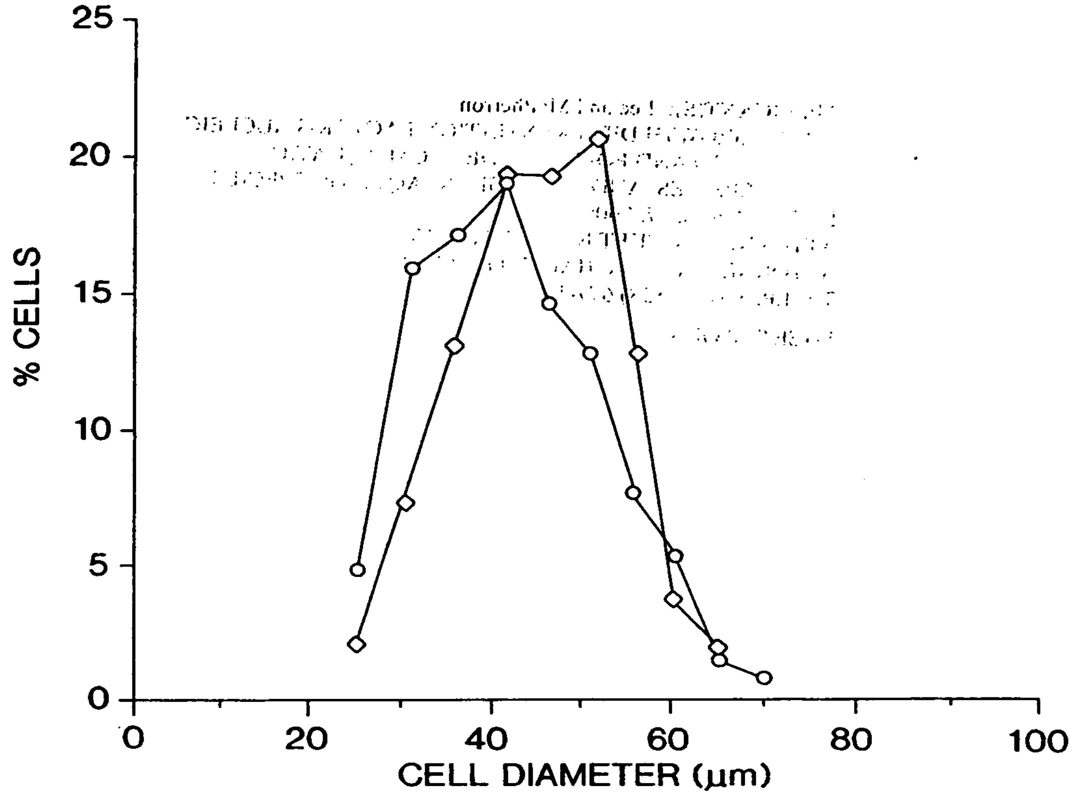


FIG. 13A

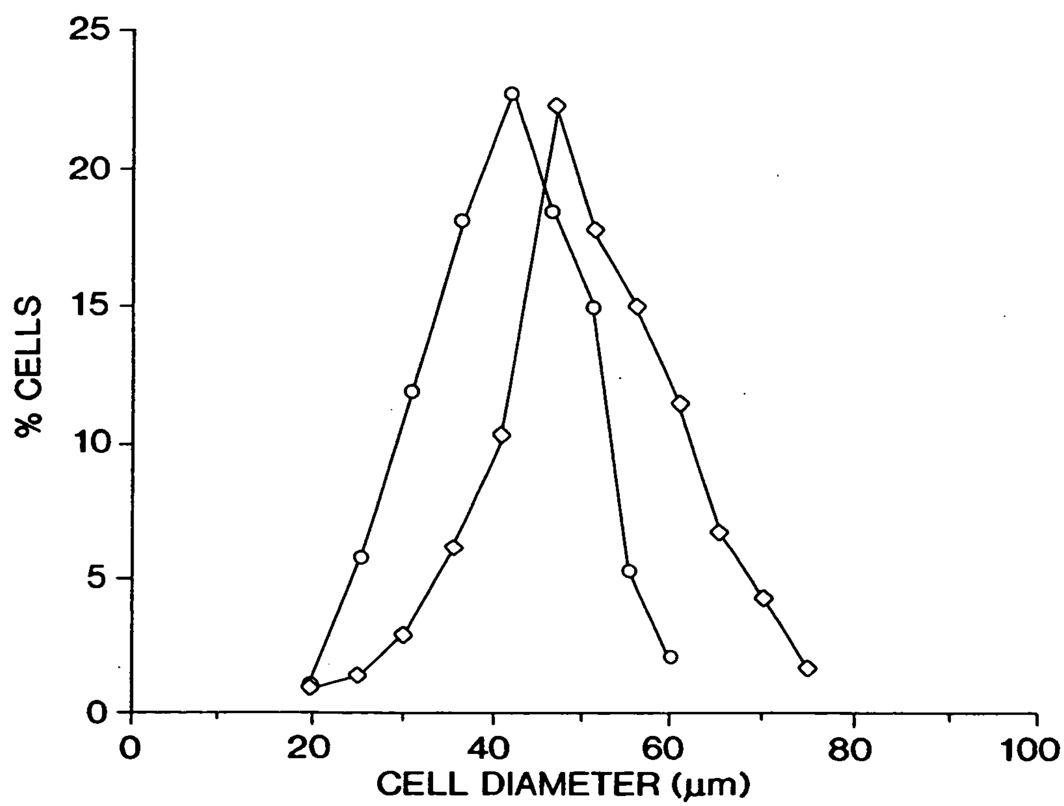


FIG. 13B

Cod DNA
[Strand]

```
1    ACTCCCCCGAGTCCCGGTGCTGCCGCTACCCCCTCACAGTGGACTTTGAAGACTTTGGCTGGGACTGGGTGATCGCGCCCAAGCG
      S  P  E  S  R  C  C  R  Y  P  L  T  V  D  F  E  D  F  G  W  D  W  V  I  A  P  K  R

86   ATACAAGGCCAACTATTGCTCCGGGGAGTGTGAGTACATGTACCTGCAGAAGTACCCCCACACCCACCTGGTGCACAAGGCCAGC
      Y  K  A  N  Y  C  S  G  E  C  E  Y  M  Y  L  Q  K  Y  P  H  T  H  L  V  H  K  A  S

171  CCCCGGGGCAACGCTGGGCCCTGCTGCACGCCCACCAAGATGTCCCCCATCAACATGCTCTACTTCAACCGCAAGGAGCAGATCA
      P  R  G  N  A  G  P  C  C  T  P  T  K  M  S  P  I  N  M  L  Y  F  N  R  K  E  Q  I

256  TCTACGGCAAGCTGCCCTCTATGGTCGTA
     I  Y  G  K  L  P  S  M  V  V
```

FIG. 14

Sea Bass
[Strand]

```
1    TGCTGCCGCTACCCACTCACAGTGGACTTTGAAGACTTTGGTTGGGACTGGATTATTGCCCCAAAGCGCTACAAGGCCAACTATT
      C  C  R  Y  P  L  T  V  D  F  E  D  F  G  W  D  W  I  I  A  P  K  R  Y  K  A  N  Y

86   GCTCCGGGGAGTGTGAGTACATGCACTTGCAGAAGTATCCGCACACCCACCTGGTGAACAAAGCCAACCCCAGAGGGACCGCGGG
     C  S  G  E  C  E  Y  M  H  L  Q  K  Y  P  H  T  H  L  V  N  K  A  N  P  R  G  T  A  G

171  TCCCTGCTGCACCCCGACCAAGATGTCGCCCATNAACATGCTCTACTTTAACCGAAAAGAGCAGATAATCTACGGCAAGATCCCT
       P  C  C  T  P  T  K  M  S  P  ?  N  M  L  Y  F  N  R  K  E  Q  I  I  Y  G  K  I  P

256  TCCATGGTGGTG
      S  M  V  V
```

FIG. 15

Sea Bream DNA
[Strand]

```
1    TCTCAGAGTCCCGGTGCTGCCGCTACCCGCTCACGGTGGACTTCGAAGACTTTGGCTGGGACTGGATTATTGCCCCAAAGCGCTA
       S  E  S  R  C  C  R  Y  P  L  T  V  D  F  E  D  F  G  W  D  W  I  I  A  P  K  R  Y

86   CAAGGCCAACTATTGCTCCGGGGAGTGTGAGTACATGCACTTGCAGAAGTACCCGCACACCCACCTGGTGAACAAAGCCAACCCC
      K  A  N  Y  C  S  G  E  C  E  Y  M  H  L  Q  K  Y  P  H  T  H  L  V  N  K  A  N  P

171  AGAGGGTCCGCGGGCCCCTGCTGTACCCCCACCAAGATGTCGCCCATCAACATGCTCTACTTTAACCGAAAGGAGCAGATCATCT
      R  G  S  A  G  P  C  C  T  P  T  K  M  S  P  I  N  M  L  Y  F  N  R  K  E  Q  I  I

256  ACGGCAAGATCCCGTCCATGGTGGTA
     Y  G  K  I  P  S  M  V  V
```

FIG. 16

Tautog DNA
[Strand]

1 CTCAGAGTCCCGGTGCTGCCGCTACCCACTCACAGTGGACTTTGAAGACTTTGGCTGGGACTGGATTATTGCTCCAAAGCGCTAC
S E S R C C R Y P L T V D F E D F G W D W I I A P K R Y

86 AAGGCCAACTATTGCTCCGGGGAGTGTGAGTACATGCACCTGCAGAAGTACCCGCACACCCACCTCGTGAACAAAGCCAACCCCA
K A N Y C S G E C E Y M H L Q K Y P H T H L V N K A N P

171 GAGGGACTGCAGGCCCCTGCTGCACCCCCACCAAGATGTCGCCCATCAACATGCTCTACTTTAACCGAAAGGAGCAGATCATCTA
R G T A G P C C T P T K M S P I N M L Y F N R K E Q I I Y

256 CGGCAAGATCCCCTCCATGGTGGTG
G K I P S M V V

FIG. 17

X. laevis T7

[Strand]

```
1    TCCAAAACGATATAAAGCCAACTATTGCTCTGGAGAGTGCGGCATTGTCTTTTTGCAAAAGTACCCGCACACACATCTTGTTCAA
      P  K  R  Y  K  A  N  Y  C  S  G  E  C  G  I  V  F  L  Q  K  Y  P  H  T  H  L  V  Q

86   CAAGCAAACCCCAGAGGTTCTGCTGGCCCTTGCTGTACCCCAACCAAAATGTCCCCAATTAATATGTTGTATTTCAATGAAAATG
      Q  A  N  P  R  G  S  A  G  P  C  C  T  P  T  K  M  S  P  I  N  M  L  Y  F  N  E  N

171  AACAAATCATATATGGAAAAATTCCAGCTATGGTGGTA
     E  Q  I  I  Y  G  K  I  P  A  M  V  V
```

FIG. 18

```
                                  10                  20                  30
humanMSTN   C C R Y P L T V D F E A F G W D W I I A P K R Y K A N Y C S   33
Zebrafish   C C R Y P L T V D F E D F G W D W I I A P K R Y K A N Y C S   44
Salmon      C C R Y P L T V D F E D F G W D W I I A P K R Y K A N Y C S   44
Cod         C C R Y P L T V D F E D F G W D W V I A P K R Y K A N Y C S   35
Sea Bass    C C R Y P L T V D F E D F G W D W I I A P K R Y K A N Y C S   30
Sea Bream   C C R Y P L T V D F E D F G W D W I I A P K R Y K A N Y C S   34
Tautog      C C R T P L T V D F E D F G W D W I I A P K R Y K A N Y C S   34
X. laevis   - - - - - - - - - - - - - - - - - - - - P K R Y K A N Y C S   10

                                  40                  50                  60
humanMSTN   G E C E F V F L Q K Y P H T H L V H Q A N P R G S A G P C C   63
Zebrafish   G E C D Y M Y L Q K Y P H T H L V N K A S P R G T A G P C C   74
Salmon      G E C E Y M H L Q K Y P H T H L V N K A N P R G T A G P C C   74
Cod         G E C E Y M Y L Q K Y P H T H L V H K A S P R G N A G P C C   65
Sea Bass    G E C E Y M H L Q K Y P H T H L V N K A N P R G T A G P C C   60
Sea Bream   G E C E Y M H L Q K Y P H T H L V N K A N P R G S A G P C C   64
Tautog      G E C E Y M H L Q K Y P H T H L V N K A N P R G T A G P C C   64
X. laevis   G E C G I V F L Q K Y P H T H L V Q Q A N P R G S A G P C C   40

                                  70                  80                  90
humanMSTN   T P T K M S P I N M L Y F N G K E Q I I Y G K I P A M V V     92
Zebrafish   T P T K M S P I N M L Y F N G K E Q I I Y G K I P S M V V     103
Salmon      T P T K M S P I N M L Y F N R K E Q I I Y G K I P S M V V     103
Cod         T P T K M S P I N M L Y F N R K E Q I I Y G K L P S M V V     94
Sea Bass    T P T K M S P X N M L Y F N R K E Q I I Y G K I P S M V V     89
Sea Bream   T P T K M S P I N M L Y F N R K E Q I I Y G K I P S M V V     93
Tautog      T P T K M S P I N M L Y F N R K E Q I I Y G K I P S M V V     93
X. laevis   T P T K M S P I N M L Y F N E N E Q I I Y G K I P A M V V     69
```

Decoration 'Decoration #1': Shade (with solid black) residues that match humanMSTN exactly.

FIG. 19

Percent Similarity

Percent Divergence

	1	2	3	4	5	6	7	8		
1		88.8	89.9	87.6	88.8	91.0	88.8	92.8	1	humanMSTN
2	11.2		95.5	93.3	94.4	94.4	94.4	84.1	2	Zebrafish
3	10.1	4.5		93.3	98.9	98.9	98.9	85.5	3	Salmon
4	12.4	6.7	6.7		92.1	93.3	92.1	82.6	4	Cod
5	10.2	4.5	0.0	6.8		97.8	97.8	84.1	5	Sea Bass
6	9.0	5.6	1.1	6.7	1.1		97.8	87.0	6	Sea Bream
7	11.2	5.6	1.1	7.9	1.1	2.2		85.5	7	Tautog
8	7.2	15.9	14.5	17.4	14.7	13.0	14.5		8	X. laevis
	1	2	3	4	5	6	7	8		

FIG. 20

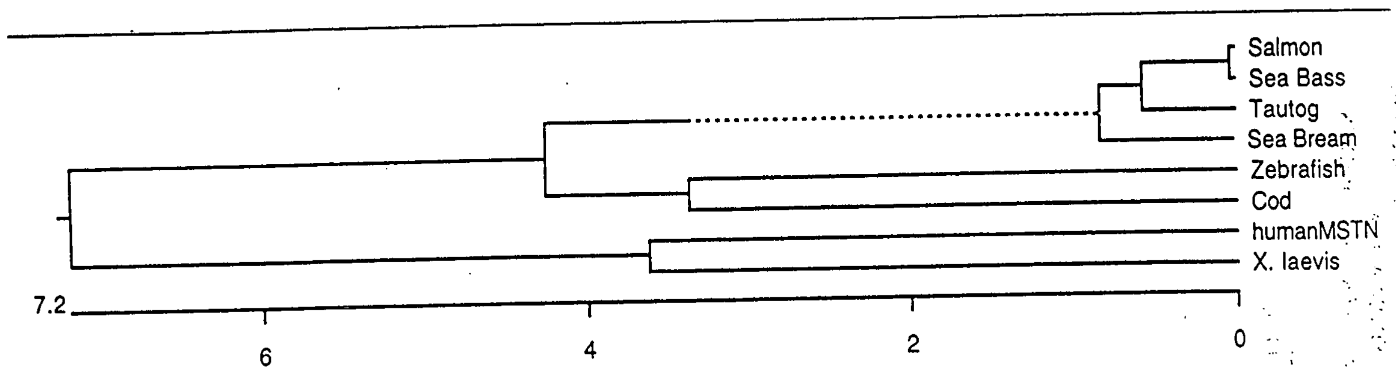

Salmon
Sea Bass
Tautog
Sea Bream
Zebrafish
Cod
humanMSTN
X. laevis
7.2
6
4
2
0

FIG. 21